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LOCUS HMEK1 NUC 3911 BP DS-

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1 CGGCCTGGAA GCACGAGTGG TTGGAAAGGA GAAATAGGCG AGGGCCTGTG GTGGTAAAAAC
61 CAATCCCAGT TAAAGGAGAT GGATCTGAAA TGAATCACTT AGCAGCTGAG TCTCCAGGAG
121 AGGTCCAGGC AAGTGC GGCT TCACCAGCTT CCAAAGGCCG ACGCAGTCCT TCTCCTGGCA
181 ACTCCCCATC AGGTGCGACA GTGAAATCAG AATCTCCAGG AGTAAGGAGA AAAAGAGTTT
241 CCCCAGTGCC TTTTCAGAGT GGCAGAATCA CACCACCCCG AAGAGCCCCT TCACCAGATG
301 GCTTCTCACC ATATAGCCCT GAGGAAACAA ACCGCCGTGT TAACAAAGTG ATGCGGGCCA
361 GACTGTACTT ACTGCAGCAG ATAGGGCCTA ACTCTTTCCT GATTGGAGGA GACAGCCCAG
421 ACAATAAATA CCGGGTGT TTATTGGGCCTC AGAACTGCAG CTGTGCACGT GGAACATTCT
481 GTATTTCATCT GCTATTTGTG ATGCTCCGGG TGTTCCTCACT AGAACCTTCA GACCCAATGT
541 TATGGAGAAA AACTTTAAAG AATTTTGAGG TTGAGAGTTT GTTCCAGAAA TATCACAGTA
601 GCGTAGCTC AAGGATCAAA GCTCCATCTC GTAACACCAT CCAGAAGTTT GTTTCACGCA
661 TGTCAAATTC TCATACATTC GTATCATCTA GTACTTCTAC ATCTAGTTCA GTAAACAGCA
721 TAAAGGATGA AGAGGAACAG ATGTGTCCTA TTTGCTTGTT GGGCATGCTT GATGAAGAAA
781 GTCTTACAGT GTGTGAAGAC GGCTGCAGGA ACAAGCTGCA CCACCACTGC ATGTCAATTT
841 GGGCAGAGA GTGTAGAAGA AATAGAGAAC CTTTAATATG TCCCTTTTGT AGATCTAAGT
901 GGAGATCTCA TGATTTCTAC AGCCACGAGT TGTCAAGTCC TGTGGATTCC CCTTCTTCCC
961 TCAGAGCTGC ACAGCAGCAA ACCGTACAGC AGCAGCCTTT GGCTGGATCA CGAAGGAATC
1021 AAGAGAGCAA TTTTAACCTT ACTCATTATG GAACTCAGCA AATCCCTCCT GCTTACAAAG
1081 ATTTAGCTGA GCCATGGATT CAGGTGTTTG GAATGGAACG CGTTGGCTGC TTATTCTCTA
1141 GAACTGGAA CGTAAGGGAA ATGGCCCTTA GCGCTCTTTC CCACGACGTT AGTGGGGCCC
1201 TGTGTTGGC AAACGGGGAG AGCACTGGAA ACTCTGGAGG CCGCAGTGGG GGCAGCTTAA
1261 GCGCGGGAGC GGCCAGCGGG TCCTCCCAGC CCAGCATCTC AGGGGATGTG GTGGAGGCGT
1321 GCTGCAGTGT CCTGTCTATA GTCTGCGTGT ACCCTGTCTA CAAAGTGTAC GTTGTGCTTT
1381 TAAAAACATT GAGAGCCATG CTGGTATACA CTCTTGCCA CAGTCTGGCA GAAAGAATCA
1441 AACTTCAGAG ACTCCTCCGG CCAGTTGTAG ACACTATCCT TGTCAAGTGT GCAGATGCCA
1501 ACAGCCGAC GAGTCAGCTG TCCATATCTA CAGTGTCTGA ACTCTGCAAT GGCCAAGCAG
1561 GAAAGCTGGC GGTGAGGAGA GAAATACCTA AAGCTGGGTC CATCGGGGTT GGTGGTGTCTG
1621 ATTACGTCTT AAGTTGTATC CTTGGAACCC AAGCTGAATC AAACAAGTGG CAAGAAGTGC
1681 TGGGTGCGCT TTGTCTTATA GACAGGTTGC TGTGGAATT TCCTGCTGAA TTCTATCCTC
1741 ATATTGTCTG TACTGATGTC TCACAAGCTG AGCCTGTTGA AATCAGGTAC AAGAAGCTGC
1801 TCTCCCTCTT AACCTTTGCC TTGCAATCCA TTGACAATTC CCACTCGATG GTTGCAAGC
1861 TCTCTCGGAG GATATATCTG AGCTCTGCCA GGATGGTGAC CGCAGTGCCC GCTGTGTTTT
1921 CCAAGCTGGT AACCATGCTT AATGCTTCTG GCTCCACCCA CTTACCAGG ATGCGCCGGC
1981 GTCTGATGGC TATCGCGGAT GAGGTAGAAA TTGCCGAGG CATCCAGCTG GGTGTGGAGG
2041 ACAGTGTGGA TGGGCATCAG GACAGCTTAC AGGCGCTGGC CCCCAGCAGC TGTCTAGAAA
2101 ACAGCTCCCT TGAGCACACA GTCCATAGAG AGAAAAGTGG AAAAGGACTA AGTGCTACGA
2161 GACTGAGTGC CAGCTCGGAG GACATTTCTG ACAGACTGGC CCGCGTCTCT GTAGGACTTC
2221 CCAGCTCAAC AACAACAGAA CAACCAAAGC CAGCGGTTCA AACAAAAGGC AGACCCACA
2281 GTCAGTGTTC GAACTCCTCC CCTTTGTCTC ATGCTCAATT AATGTTCCCA GCACCATCAG
2341 CCCCTTGTTC CTCTGCCCGG TCTGTCCCAG ATATTTCTAA GCACAGACCC CAGGCATTTG
2401 TTCCCTGCAA AATACCTTCC GCATCTCCTC AGACACAGCG CAAGTTCTCT CTACAATTCC
2461 AGAGGAACTG CTCTGAACAC CGAGACTCAG ACCAGCTCTC CCCAGTCTC ACTCAGTCAA
2521 GACCCCAACC CTCCAGTAAC ATACACAGGC CAAAGCCATC CCGACCCGTT CCGGGCAGTA
2581 CAAGCAAACCT AGGGGACGCC AAAAAAGTA GCATGACACT TGATCTGGGC AGTGCTTCCA
2641 GGTGTGACGA CAGCTTTGGC GCGCGCGGCA ACAGTGGCAA CGCCGTCATA CCCAGCGACG
2701 AGACAGTGTG CAGCCCGGTG GAGGACAAGT GCAGGTTAGA TGTGAACACC GAGCTCAACT
2761 CCAGCATCGA GGACCTTCTT GAAGCATCCA TGCCTTCAAG TGACACGACA GTCATTCTCA
2821 AGTCCGAAGT CGCCGTCCTC TCTCCGGAAA AGGCCGAAA TGACGACACC TACAAAGACG
2881 ACGTCAATCA TAATCAAAAG TGCAAAAGAA AGATGGAAGC TGAAGAGGAG GAGGCTTTAG
2941 CGATCGCCAT GGCGATGTCA GCGTCTCAGG ATGCCCTCCC CATCGTCCCT CAGCTGCAGG
3001 TGGAAAAATGG AGAAGATATT ATCATCATTC AGCAGGACAC ACCAGAAACT CTTCCAGGAC
3061 ATACCAAAGC GAAACAGCCT TACAGAGAAG ACGCTGAGTG GCTGAAAGGC CAGCAGATAG
3121 GCCTCGGAGC ATTTCTTCT TGTATCAGG CTCAAGATGT GGGAACTGGA ACTTTAATGG
3181 CTGTTAAACA GGTGACTTAT GTCAGAAACA CATCTTCTGA GCAAGAAGAA GTAGTAGAAG
3241 CACTAAGAGA AGAGATAAGA ATGATGAGCC ATCTGAATCA TCCAAACATC ATTAGGATGT
3301 TGGGAGCCAC GTGTGAGAAG AGCAATTACA ATCTCTTCAT TGAATGGATG GCAGGGGGAT

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FIGURE 1A

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3361 CCGTGGCTCA TTTGCTGAGT AAATATGGAG CCTTCAAAGA ATCAGTAGTT ATTA ACTACA  
3421 CTGAACAGTT ACTCCGTGGC CTTTCGTATC TCCATGAGAA CCAGATCATT CACAGAGATG  
3481 TCAAAGGTGC CAATTTGCTC ATTGACAGCA CCGGTCAGAG GCTGAGAATT GCAGACTTTG  
3541 GAGCTGCAGC CAGGTTGGCA TCAAAGGAA CTGGTGCAGG AGAGTTTCAG GGACAATTAC  
3601 TGGGGACAAT TGCATTCATG GCGCCTGAGG TCCTAAGAGG TCAGCAGTAT GGTAGGAGCT  
3661 GTGATGTATG GAGTGTTGGC TGCGCCATTA TAGAAATGGC TTGTGCAAAA CCACCTTGGA  
3721 ATGCAGAAAA AACTCCAAT CATCTCGCCT TGATATTTAA GATTGCTAGC GCAACTACTG  
3781 CACCGTCCAT CCCGTCACAC CTGTCCCTG GTTTACGAGA TGTGGCTCTT CGTTGTTTAG  
3841 AACTTCAGCC TCAGGACCGG CCTCCGTCAA GAGAGCTGCT GAAACATCCG GTCTTCCGTA  
3901 CCACGTGGTA G

FIGURE 1B

000050 52020700

## Mouse MEKK1 cDNA

10 20 30 40  
GCC CGC GAG AGA AAA TGG CGG CGG CGG CGC GCG ATC CCG CCT CGT  
CGG GCG CTC TCT TTT ACC GCC GCC GCC CGC TAG CGC GGA GCA

50 60 70 80 90  
CGT CGG GAT TCC CGG GCG CCG CGG CGG CGA GTC CCG AGG CGG CCG  
GCA GCC CTA AGG GCC CGC GGC GCC GCC GCT CAG GGC TCC GCC CGC

100 110 120 130  
GCG GCG GCG GAG GAG GAG GAG CTC TCC AGG GAA CCG GCG CGC CCG  
CGC CGC CGC CTC CTC CTC CTC GAG AGG TCC CTT CGC CGC GCG GGC

140 150 160 170 180  
CAG CGG GCG CGG CGG GGC TGC TGC GGC AGC CTG GCA GCG CGG GCC  
GTC GCC CGC GCC GCC CCG ACG ACG CCC TCG GAC CGT CGC GCC CGG

190 200 210 220  
GCG AGC GCG CGG ACT GGC GGC GGC GGC AGC TGC GCA AAG TGC GGA  
CGC TCG CGC GCC TGA CCG CCG CCG CCG TCG ACG CGT TTC ACG CCT

230 240 250 260 270  
GTG TGG AGC TGG ACC AGC TGC CCG AGC AGC CGC TCT TCC TCG CCG  
CAC ACC TCG ACC TGG TCG ACG GCC TCG TCG GCG AGA AGG AGC GGC

280 290 300 310  
CCG CCT CGC CGC CCT GCC CAT CTA CTT CCC CGT CGC CGG AGC CCG  
GGC GGA GCG GCG GGA CGG GTA GAT GAA GGG GCA GCG GCC TCG GGC

320 330 340 350 360  
CGG ACG CGG CTG CAG GAG CGA GTC GCT TCC AGC CCG CGG CGG GAC  
GCC TCG GCC GAC GTC CTC GCT CAG CGA AGG TCG GGC GCC GCC CTG

370 380 390 400  
CGC CAC CCC CGG GAG CGG CGA GTC GCT GCG GCT CCC ACT CTG CCG  
GCG GTG GGG GCC CTC GCC GCT CAG CGA CGC CGA GCG TGA GAC GGC

410 420 430 440 450  
AGC TGG CGG CCG CGC GGG ACA GCG GCG CCC GGA GCC CCG CGG GGG  
TCG ACC GCC GGC GCG CCC TGT CGC CGC GGG CCT CGG GGC GCC CCC

460 470 480 490  
CCG AGC CGC CCT CTG CAG CGG CCC CCT CCG GTC GAG AGA TGG AGA  
GGC TCG GCG GGA GAC GTC GCC GGG CGA GGC CAG CTC TCT ACC TCT

500 510 520 530 540  
.

FIGURE 2A



## Mouse MEKK1 cDNA

1040 1050 1060 1070 1080  
ACT GCA OCT GTG GGC GTG GAG CAT TCT GTA TTC ACC TCT TGT TTG  
TGA CGT CGA CAC CCG CAC CTC GTA AGA CAT AAG TGG AGA ACA AAC

1090 1100 1110 1120  
TCA TGC TCC GGG TGT TTC AGC TAG AAC CCT CTG ACC CCA TGT TAT  
AGT ACG AGG CCC ACA AAG TCG ATC TTG GGA GAC TGG GGT ACA ATA

1130 1140 1150 1160 1170  
GGA GAA AAA CTT TAA AAA ATT TCG AGG TTG AGA GTT TGT TCC AGA  
CCT CTT TTT GAA ATT TTT TAA AGC TCC AAC TCT CAA ACA AGG TCT

1180 1190 1200 1210  
AAT ACC ACA GTA GGC GTA GCT CGA GAA TCA AAG CTC CAT CCC GGA  
TTA TGG TGT CAT CCG CAT CGA GCT CTT AGT TTC GAG GTA GGG CCT

1220 1230 1240 1250 1260  
ACA CCA TCC AGA AGT TTG TGT CAC GCA TGT CAA ATT CTC ACA CAC  
TGT GGT AGG TCT TCA AAC ACA GTG CGT ACA GTT TAA GAG TGT GTG

1270 1280 1290 1300  
TGT CAT CGT CTA GCA CAT CCA CAT CTA GTT CAG AAA ACA GCA TCA  
ACA GTA GCA GAT CGT GTA GGT GTA GAT CAA GTC TTT TGT CGT AGT

1310 1320 1330 1340 1350  
AGG ATG AAG AGG AGC AGA TOT GTC CCA TCT GCT TGC TGG GCA TGC  
TCC TAC TTC TCC TCG TCT ACA CAG GGT AGA CGA ACG ACC CGT ACC

1360 1370 1380 1390  
TGG ATG AGG AGA GCC TGA CTG TGT GTG AAG ATG GCT GCA GGA ACA  
ACC TAC TCC TCT CCG ACT GAC ACA CAC TTC TAC CGA CGT CCT TGT

1400 1410 1420 1430 1440  
AGC TGC ACC ACC ATT GCA TGT CCA TCT GGG CGG AAG AGT GTA GAA  
TCG ACG TGG TGG TAA CGT ACA GGT AGA CCC GCC TTC TCA CAT CTT

1450 1460 1470 1480  
GAA ATA GAG AGC CTT TAA TAT GTC CCC TTT GTA GAT CTA AGT GGA  
CTT TAT CTC TCG GAA ATT ATA CAG GGG AAA CAT CTA GAT TCA CCT

1490 1500 1510 1520 1530  
GAT CCC ATG ACT TCT ACA GCC ATG AGT TAT CAA GCC CCG TGG AGT  
CTA GGG TAC TGA AGA TGT CGG TAC TCA ATA GTT CGG GGC ACC TCA

1540 1550 1560 1570

FIGURE 2C

### Mouse MEKK1 cDNA

CCC CCG CCT CCC TGC GAG CTG TCC AGC AGC CAT CCT CCC CCG AGC  
GGG GGC GGA GGG ACG CTC GAC AGG TCG TCG GTA GGA GGG GCG TCG

1580 1590 1600 1610 1620  
AGC CCG TGG CCG GAT CAC AGC GGA GGA ATC AGG AGA GCA GTT TTA  
TCG GGC ACC GGC CTA GTG TCG CCT CCT TAG TCC TCT CGT CAA AAT

1630 1640 1650 1660  
ACC TTA CTC ATT TTG GAA CCC AGC AGA TTC CTT CCG CTT ACA AAG  
TGG AAT GAG TAA AAC CTT GGG TCG TCT AAG GAA GGC GAA TGT TTC

1670 1680 1690 1700 1710  
ATT TGG CCG AGC CAT GGA TTC AGG TGT TTG GAA TGG AAC TCG TTG  
TAA ACC GGC TCG GTA CCT AAG TCC ACA AAC CTT ACC TTG AGC AAC

1720 1730 1740 1750  
GCT GCT TAT TCT CTA GAA ACT GGA ACG TAA GGG AAA TGG CCC TTA  
CGA CGA ATA AGA GAT CTT TGA CCT TGC ATT CCC TTT ACC GGG AAT

1760 1770 1780 1790 1800  
GGC GTC TTT CCC ACG ACG TTA GTG GGG CCC TGT TGT TGG CAA ACG  
CCG CAG AAA GGG TGC TGC AAT CAC CCC GGG ACA ACA ACC GTT TCG

1810 1820 1830 1840  
GGG AGA GCA CTG GAA ACT CTG GAG GCG GCA GTG GGG GCA GCT TAA  
CCC TCT CGT GAC CTT TGA GAC CTC GCG CGT CAC CCC CGT CGA ATT

1850 1860 1870 1880 1890  
GCG CCG GAG CCG CCA GCG GGT CCT CCC AGC CCA GCA TCT CAG GGG  
CGC GCC CTC GCC GGT CGC CCA GGA GGG TCG GGT CGT AGA GTC CCC

1900 1910 1920 1930  
ATG TGG TGG AGG CGT GCT GCA GTG TCC TGT CTA TAG TCT GCG CTG  
TAC ACC ACC TCC GCA CGA CGT CAC AGG ACA GAT ATC AGA CCG GAC

1940 1950 1960 1970 1980  
ACC CTG TCT ACA AAG TGT ACG TTG CTG CTT TAA AAA CAT TGA GAG  
TGG GAC AGA TGT TTC ACA TGC AAC GAC GAA ATT TTT GTA ACT CTC

1990 2000 2010 2020  
CCA TGC TGG TAT ACA CTC CTT GCC ACA GTC TGG CAG AAA GAA TCA  
GGT ACG ACC ATA TGT GAG GAA CGG TGT CAG ACC GTC TTT CTT AGT

2030 2040 2050 2060 2070  
AAC TTC AGA GAC TCC TCC GGC CAG TTG TAG ACA CTA TCC TTG TCA

FIGURE 2D

## Mouse MEKK1 cDNA

TTG AAG TCT CTG AGG AGG CCG GTC AAC ATC TGT GAT AGG AAC AGT  
2080 2090 2100 2110  
ACT GTG CAG ATG CCA ACA GCC GCA CGA GTC AGC TGT CCA TAT CTA  
TCA CAC GTC TAC GGT TGT CCG CGT GCT CAG TCG ACA GGT ATA GAT  
2120 2130 2140 2150 2160  
CAG TGC TGG AAC TCT GCA AGG GCC AAG CAG GAG AGC TGG CCG TTG  
GTC ACG ACC TTG AGA CGT TCC CGG TTC GTC CTC TCG ACC GCC AAC  
2170 2180 2190 2200  
GGA GAG AAA TAC TTA AAG CTG GGT CCA TCG GGG TTG GTG GTG TCG  
CCT CTC TTT ATG AAT TTC GAC CCA GGT AGC CCC AAC CAC CAC AGC  
2210 2220 2230 2240 2250  
ATT ACG TCT TAA GTT GTA TCC TTG GAA ACC AAG CTG AAT CAA ACA  
TAA TGC AGA ATT CAA CAT AGG AAC CTT TGG TTC GAC TTA GTT TGT  
2260 2270 2280 2290  
ACT GGC AAG AAC TGC TGG GTC GCC TCT GTC TTA TAG ACA GGT TGC  
TGA CCG TTC TTG ACG ACC CAG CGG AGA CAG AAT ATC TGT CCA ACG  
2300 2310 2320 2330 2340  
TGT TGG AAT TTC CTG CTG AAT TCT ATC CTC ATA TTG TCA GTA CTG  
ACA ACC TTA AAG GAC GAC TTA AGA TAG GAG TAT AAC AGT CAT GAC  
2350 2360 2370 2380  
ATG TCT CAC AAG CTG AGC CTG TTG AAA TCA GGT ACA AGA AGC TGC  
TAC AGA GTG TTC GAC TCG GAC AAC TTT AGT CCA TGT TCT TCG ACG  
2390 2400 2410 2420 2430  
TCT CCC TCT TAA CCT TTG CCT TGC AAT CCA TTG ACA ATT CCC ACT  
AGA GGG AGA ATT GGA AAC GGA ACG TTA GGT AAC TGT TAA GGG TGA  
2440 2450 2460 2470  
CGA TGG TTG GCA AGC TCT CTC GGA GGA TAT ATC TGA GCT CTG CCA  
GCT ACC AAC CGT TCG AGA GAG CCT CCT ATA TAG ACT CGA GAC GGT  
2480 2490 2500 2510 2520  
GGA TGG TGA CCG CAG TGC CCG CTG TGT TTT CCA AGC TGG TAA CCA  
CCT ACC ACT GGC GTC ACG GGC GAC ACA AAA GGT TCG ACC ATT GGT  
2530 2540 2550 2560  
TGC TTA ATG CTT CTG GCT CCA CCC ACT TCA CCA GGA TGC GCC GGC  
ACG AAT TAC GAA GAC CGA GGT GGG TGA AGT GGT CCT ACG CCG CCG

FIGURE 2E

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## Mouse MEKK1 cDNA

2570 2580 2590 2600 2610  
\* \* \* \* \*  
GTC TGA TGG CTA TCG CGG ATG AGG TAG AAA TTG CCG AGG TCA TCC  
CAG ACT ACC GAT AGC GCC TAC TCC ATC TTT AAC GGC TCC AGT AGG

2620 2630 2640 2650  
\* \* \* \* \*  
AGC TGG GTG TGG AGG ACA CTG TGG ATG GGC ATC AGG ACA GCT TAC  
TCG ACC CAC ACC TCC TGT GAC ACC TAC CCG TAG TCC TGT CGA ATG

2660 2670 2680 2690 2700  
\* \* \* \* \*  
AGG CCG TGG CCC CCA CCA GCT GTC TAG AAA ACA GCT CCC TTG AGC  
TCC GGC ACC GGG GGT GGT CGA CAG ATC TTT TGT CGA GGG AAC TCG

2710 2720 2730 2740  
\* \* \* \* \*  
ACA CAG TCC ATA GAG AGA AAA CTG GAA AAG GAC TAA GTG CTA CGA  
TGT GTC AGG TAT CTC TCT TTT GAC CTT TTC CTG ATT CAC GAT GCT

2750 2760 2770 2780 2790  
\* \* \* \* \*  
GAC TGA GTG CCA GCT CGG AGG ACA TTT CTG ACA GAC TGG CCG GCG  
CTG ACT CAC GGT CGA GCC TCC TGT AAA GAC TGT CTG ACC GGC CGC

2800 2810 2820 2830  
\* \* \* \* \*  
TCT CTG TAG GAC TTC CCA GCT CAA CAA CAA CAG AAC AAC CAA AGC  
AGA GAC ATC CTG AAG GGT CGA GTT GTT GTT GTC TTG TTG GTT TCG

2840 2850 2860 2870 2880  
\* \* \* \* \*  
CAG CGG TTC AAA CAA AAG GCA GAC CCC ACA GTC AGT GTT TGA ACT  
GTC GCC AAG TTT GTT TTC CGT CTG GGG TGT CAG TCA CAA ACT TGA

2890 2900 2910 2920  
\* \* \* \* \*  
CCT CCC CTT TGT CTC ATG CTC AAT TAA TGT TCC CAG CAC CAT CAG  
GGA GGG GAA ACA GAG TAC GAG TTA ATT ACA AGG GTC GTG GTA GTC

2930 2940 2950 2960 2970  
\* \* \* \* \*  
CCC CTT GTT CCT CTG CCC CGT CTG TCC CAG ATA TTT CTA AGC ACA  
GGG GAA CAA GGA GAC GGG GCA GAC AGG GTC TAT AAA GAT TCG TGT

2980 2990 3000 3010  
\* \* \* \* \*  
GAC CCC AGG CAT TTG TTC CCT GCA AAA TAC CTT CCG CAT CTC CTC  
CTG GGG TCC GTA AAC AAG GGA CGT TTT ATG GAA GGC GTA GAG GAG

3020 3030 3040 3050 3060  
\* \* \* \* \*  
AGA CAC AGC GCA AGT TCT CTC TAC AAT TCC AGA GGA ACT GCT CTG  
TCT GTG TCG CGT TCA AGA GAG ATG TTA AAG TCT CCT TGA CGA GAC

3070 3080 3090 3100  
\* \* \* \* \*

FIGURE 2F



## Mouse MEKK1 cDNA

AAC ACC GAG ACT CAG ACC AGC TCT CCC CAG TCT TCA CTC AGT CAA  
TTG TGG CTC TGA GTC TGG TCG AGA GGG GTC AGA AGT GAG TCA GTT

3110 3120 3130 3140 3150  
GAC CCC CAC CCT CCA GTA ACA TAC ACA GGC CAA AGC CAT CCC GAC  
CTG GGG GTG GGA GGT CAT TGT ATG TGT CCG GTT TCG GTA GGG CTG

3160 3170 3180 3190  
CCG TTC CGG GCA GTA CAA GCA AAC TAG GGG ACG CCA CAA AAA GTA  
GGC AAG GCC CGT CAT GTT CGT TTG ATC CCC TGC GGT GTT TTT CAT

3200 3210 3220 3230 3240  
GCA TGA CAC TTG ATC TGG GCA GTG CTT CCA GGT GTG ACG ACA GCT  
CGT ACT GTG AAC TAG ACC CGT CAC GAA GGT CCA CAC TGC TGT CGA

3250 3260 3270 3280  
TTG GCG GCG GCG GCA ACA GTG GCA ACG CCG TCA TAC CCA GCG ACG  
AAC CGC CGC CGC CGT TGT CAC CGT TGC GGC AGT ATG GGT CGC TGC

3290 3300 3310 3320 3330  
AGA CAG TGT TCA CGC CGG TGG AGG ACA AGT GCA GGT TAG ATG TGA  
TCT GTC ACA AGT GCG GCC ACC TCC TGT TCA CGT CCA ATC TAC ACT

3340 3350 3360 3370  
ACA CCG AGC TCA ACT CCA GCA TCG AGG ACC TTC TTG AAG CAT CCA  
TGT GGC TCG AGT TGA GGT CGT AGC TCC TGG AAG AAC TTC GTA GGT

3380 3390 3400 3410 3420  
TGC CTT CAA GTG ACA CGA CAG TCA CTT TCA AGT CCG AAG TCG CCG  
ACG GAA GTT CAC TGT GCT GTC AGT GAA AGT TCA GGC TTC AGC GGC

3430 3440 3450 3460  
TCC TCT CTC CGG AAA AGG CCG AAA ATG ACG ACA CCT ACA AAG ACG  
AGG AGA GAG GCC TTT TCC GGC TTT TAC TGC TGT GGA TGT TTC TGC

3470 3480 3490 3500 3510  
ACG TCA ATC ATA ATC AAA AGT GCA AAG AAA AGA TGG AAG CTG AAG  
TGC AGT TAG TAT TAG TTT TCA CGT TTC TTT TCT ACC TTC GAC TTC

3520 3530 3540 3550  
AGG AGG AAG CTT TAG CGA TCG CCA TGG CGA TGT CAG CGT CTC AGG  
TCC TCC TCC GAA ATC GCT AGC GGT ACC GCT ACA GTC GAG TCC

3560 3570 3580 3590 3600  
ATG CCC TCC CCA TCG TCC CTC AGC TGC AGG TGG AAA ATG GAG AAG  
TAC GGG AGG GGT AGC AGG GAG TCG ACG TCC ACC TTT TAC CTC TTC

FIGURE 2G

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## Mouse MEKK1 cDNA

3610 3620 3630 3640  
ATA TTA TCA TCA TTC AGC AGG ACA CAC CAG AAA CTC TTC CAG GAC  
TAT AAT AGT AGT AAG TCG TCC TGT GTG GTC TTT GAG AAG GTC CTG

3650 3660 3670 3680 3690  
ATA CCA AAG CGA AAC AGC CTT ACA GAG AAG ACG CTG AGT GGC TGA  
TAT GGT TTC GCT TTG TCG GAA TGT CTC TTC TGC GAC TCA CCG ACT

3700 3710 3720 3730  
AAG GCC AGC AGA TAG GCC TCG GAG CAT TTT CTT CCT GTT ACC AAG  
TTC CGG TCG TCT ATC CGG AGC CTC GTA AAA GAA GGA CAA TGG TTC

3740 3750 3760 3770 3780  
CAC AGG ATG TGG GGA CTG GGA CTT TAA TGG CTG TGA AAC AGG TGA  
GTG TCC TAC ACC CCT GAC CCT GAA ATT ACC GAC ACT TTT TCC ACT

3790 3800 3810 3820  
CGT ACG TCA GAA ACA CAT CCT CCG AGC AGG AGG AGG TGG TGG AAG  
GCA TGC AGT CTT TGT GTA GGA GGC TCG TCC TCC TCC ACC ACC TTC

3830 3840 3850 3860 3870  
CGT TGA GGG AAG AGA TCC GGA TGA TGG GTC ACC TCA ACC ATC CAA  
GCA ACT CCC TTC TCT AGG CCT ACT ACC CAG TGG AGT TGG TAG GTT

3880 3890 3900 3910  
ACA TCA TCC GGA TCC TGG GGG CCA CGT GCG AGA AGA GCA ACT ACA  
TGT AGT AGG CCT ACG ACC CCC GGT GCA GCG TCT TCT CGT TGA TGT

3920 3930 3940 3950 3960  
ACC TCT TCA TTG AGT GGA TGG CCG GAG GAT CTG TGG CTC ACC TCT  
TGG AGA AGT AAC TCA CCT ACC GCC CTC CTA GAC ACC GAG TGG AGA

3970 3980 3990 4000  
TGA GTA AAT ACG GAG CTT TCA AGG AGT CAG TCG TCA TTA ACT ACA  
ACT CAT TTA TGC CTC GAA AGT TCC TCA GTC AGC AGT AAT TGA TGT

4010 4020 4030 4040 4050  
CTG AGC AGT TAC TGC GTG GCC TTT CCT ATC TCC ACG AGA ACC AGA  
GAC TCG TCA ATG ACG CAC CGG AAA GGA TAG AGG TGC TCT TGG TCT

4060 4070 4080 4090  
TCA TTC ACA GAG ACG TCA AAG GTG CCA ACC TGC TCA TTG ACA GCA  
AGT AAG TGT CTC TGC AGT TTC CAC GGT TGG ACG AGT AAC TGT CGT

4100 4110 4120 4130 4140

FIGURE 2H

## Mouse MEKK1 cDNA

CCG GTC AGA GGC TGA GAA TTG CAG ACT TTG GAG CTG CTG CCA GGT  
GGC CAG TCT CCG ACT CTT AAC GTC TGA AAC CTC GAC GAC GGT CCA

4150 4160 4170 4180  
TGG CAT CAA AAG GAA CCG GTG CAG GAG AGT TCC AGG GAC AGT TAC  
ACC GTA GTT TTC CTT GGC CAC GTC CTC TCA AGG TCC CTG TCA ATG

4190 4200 4210 4220 4230  
TGG GGA CAA TTG CAT TCA TGG CGC CTG AGG TCC TAA GAG GTC AGC  
ACC CCT GTT AAC GTA AGT ACC GCG GAC TCC AGG ATT CTC CAG TCG

4240 4250 4260 4270  
AGT ATG GTA GGA GCT GTG ATG TAT GGA GTG TTG GCT GCG CCA TTA  
TCA TAC CAT CCT CGA CAC TAC ATA CCT CAC AAC CGA CGC GGT AAT

4280 4290 4300 4310 4320  
TAG AAA TGG CTT GTG CAA AAC CAC CTT GGA ATG CAG AAA AAC ACT  
ATC TTT ACC GAA CAC GTT TTG GTG GAA CCT TAC GTC TTT TTG TGA

4330 4340 4350 4360  
CCA ATC ATC TCG CCT TGA TAT TTA AGA TTG CTA GCG CAA CTA CTG  
GGT TAG TAG AGC GGA ACT ATA AAT TCT AAC GAT CGC GTT GAT GAC

4370 4380 4390 4400 4410  
CAC CGT CCA TCC CGT CAC ACC TGT CCC CGG GTC TCC GCG ACG TGG  
GTG GCA GGT AGG GCA GTG TGG ACA GGG GCC CAG ACG CGC TGC ACC

4420 4430 4440 4450  
CCG TGC GCT GCT TAG AAC TTC AGC CTC AGG ACC GGC CTC CGT CCA  
GGC ACG CGA CGA ATC TTG AAG TCG GAG TCC TGG CCG GAG GCA GGT

4460 4470 4480 4490 4500  
GAG AGC TGC TGA AAC ATC CGG TCT TCC GTA CCA CGT GGT AGT TAA  
CTC TCG ACG ACT TTG TAG GCC AGA AGG CAT GGT GCA CCA TCA ATT

4510 4520 4530 4540  
TTG TTC AGA TCA GCT CTA ATG GAG ACA GGA TAT GCA ACC GGG AGA  
AAC AAG TCT AGT CGA GAT TAC CTC TGT CCT ATA CGT TGG CCC TCT

4550 4560 4570 4580 4590  
GAG AAA AGA GAA CTT GTG GGC GAC CAT GCU GCT AAC CGC AGC CCT  
CTC TTT TCT CTT GAA CAC CCG CTG GTA CGG CGA TTG GCG TCG GGA

4600 4610 4620 4630  
CAC GCC ACT GAA CAG CCA GAA ACG GGG CCA GCG GGG AAC CGT ACC

FIGURE 21

## Mouse MEKK1 cDNA

GTG CGG TGA CTT GTC GGT CTT TOC CCC GGT CGC CCC TTG GCA TOG  
4640 4650 4660 4670 4680  
TAA GCA TGT GAT TGA CAA ATC ATG ACC TGT ACC TAA GCT CGA TAT  
ATT COT ACA CTA ACT GTT TAG TAC TGG ACA TGG ATT CGA GCT ATA  
4690 4700 4710 4720  
GCA GAC ATC TAC AGC TCG TOC AGG AAC TGC ACA CCG TGC CTT TCA  
CGT CTG TAG ATG TCG AGC ACG TCC TTG ACG TGT GGC ACG GAA AGT  
4730 4740 4750 4760 4770  
CAG GAC TGG CTC TGG GGG ACC AGG AAG GCG ATG GAG TTT GCA TGA  
GTC CTG ACC GAG ACC CCC TGG TCC TTC CGC TAC CTC AAA CGT ACT  
4780 4790 4800 4810  
CTA AAG AAC AGA AGC ATA AAT TTA TTT TTG GAG CAC TTT TTC AGC  
GAT TTC TTG TCT TCG TAT TTA AAT AAA AAC CTC GTG AAA AAG TCG  
4820 4830 4840 4850 4860  
TAA TCA GTA TTA CCA TGT ACA TCA ACA TGC CCG CCA CAT TTC AAA  
ATT AGT CAT AAT GGT ACA TGT AGT TGT ACG GGC GGT GTA AAG TTT  
4870 4880 4890 4900  
CTC AGA CTG TCC CAG ATG TCA AGA TCC ACT GTG TTT GAG TTT GTT  
GAG TCT GAC AGG GTC TAC AGT TCT AGG TGA CAC AAA CTC AAA CAA  
4910 4920 4930 4940 4950  
TGC AGT TCC CTC AGC TTG CTG GTA ATT GTG GTG TTT TGT TTT CGA  
ACG TCA AGG GAG TCG AAC GAC CAT TAA CAC CAC AAA ACA AAA GCT  
4960 4970 4980 4990  
TGC AAA TGT GAT GTA ATA TTC TTA TTT TCT TTG GAT CAA AGC TGG  
ACG TTT ACA CTA CAT TAT AAG AAT AAA AGA AAC CTA GTT TCG ACC  
5000 5010 5020 5030 5040  
ACT GAA AAT TGT ACT GTG TAA TTA TTT TTG TGT TTT TAA TGT TAT  
TGA CTT TTA ACA TGA CAC ATT AAT AAA AAC ACA AAA ATT ACA ATA  
5050 5060 5070 5080  
TTG GTA CTC GAA TTG TAA ATA ACG TCT ACT GCT GTT TAT TCC AGT  
AAC CAT GAG CTT AAC ATT TAT TGC AGA TGA CGA CAA ATA AGG TCA  
5090 5100 5110 5120 5130  
TTC TAC TAC CTC AGG TGT CCT ATA GAT TTT TCT TCT ACC AAA GTT  
AAG ATG ATG GAG TCC ACA GGA TAT CTA AAA AGA AGA TGG TTT CAA

FIGURE 2J

## Mouse MEKK1 cDNA

5140 5150 5160 5170  
CAC TCT CAG AAT GAA ATT CTA CGT GCT GTG TGA CTA TGA CTC CTA  
GTG AGA GTC TTA CTT TAA GAT GCA CGA CAC ACT GAT ACT GAG GAT  
5180 5190 5200 5210 5220  
AGA CTT CCA GGG CTT AAG GGC TAA CTC CTA TTA GCA CCT TAC TAT  
TCT GAA GGT CCC GAA TTC CCG ATT GAG GAT AAT CGT GGA ATG ATA  
5230 5240 5250  
GTA AGC AAA TGC TAC AAA AAA AAA AAA AAA AAA  
CAT TCG TTT ACG ATG TTT TTT TTT TTT TTT TTT

FIGURE 2K

[illegible]

### hMEKK1/mMEKK1 Protein Alignment

mouse	1	10	20	30	40
human	MAAAAGDRAS	SSGFTGAAAA	SPEAGGGGGG	GGALQGSGAP	AAGAAGLLRE
	50	60	70	80	90
mouse	FGSAGRERAD	WRRRQLRKVR	SVELDQLPEQ	PLFLAAASPP	CPSTSPSPEP
human					
	100	110	120	130	140
mouse	ADAAAGASRF	QPAAGPPPPG	AASROGSHSA	ELAAARDSGA	RSPAGAEPPS
human					
	150	160	170	180	190
mouse	AAAPSGREME	NKETLKGLHK	MEDRPEERMI	RECLKATCMP	AWKHEWLERR
human					AWKHEWLERR
	200	210	220	230	240
mouse	NRRGPFVVVKP	IPIKGDGSEV	NNLAAEPOGE	GQAGSAA PAP	KGRRSPSPGS
human	NRRGPFVVVKP	IPVKGDGSEM	NHLAAESPGE	VQASAAS PAS	KGRRSPSPGN
	250	260	270	280	290
mouse	SPSGRSVKPE	SPGVRRKRVS	FVPFQSGRIT	PERRAPSPDG	FSPYSPEETS
human	SPSGRIVKSE	SPGVRRKRVS	FVPFQSGRIT	PERRAPSPDG	FSPYSPEEIN
	300	310	320	330	340
mouse	RRVNKVMRAR	LYLLQQIGPN	SFLIGGDSPD	NKYRVFIGPQ	NCSCGRGAF
human	RRVNKVMRAR	LYLLQQIGPN	SFLIGGDSPD	NKYRVFIGPQ	NCSCARGTFC
	350	360	370	380	390
mouse	IHLFVMLRV	FQLEPSDEML	WRKTLKNFEV	ESLFQKYHSR	RSSRIKAPSR
human	IHLFVMLRV	FQLEPSDEML	WRKTLKNFEV	ESLFQKYHSR	RSSRIKAPSR
	400	410	420	430	440
mouse	NTIQKFVSRM	SNSHILSSSS	TSTSSSENSI	KDEEEQMCPI	CLLGMLDEES
human	NTIQKFVSRM	SNSHILSSSS	TSTSSSVNSI	KDEEEQMCPI	CLLGMLDEES

FIGURE 3A

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hMEKK1/mMEKK1 Protein Alignment

	450	460	470	480	490
mouse	LTVCEDGCRN	KLHHHOMSIW	AEECRNRNREP	LICPLCRSKW	RS HDFYSHEL
human	LTVCEDGCRN	KLHHHOMSIW	AEECRNRNREP	LICPLCRSKW	RS HDFYSHEL
	500	510	520	530	540
mouse	SSPVESPA SL	RAVQOPSSPQ	QPVAGSQRRN	QESS FNLTHF	GTQQIPSAVK
human	SSPVDSPS SL	RAAQQQIVQQ	QPLAGS-RRN	QESN FNLTHY	GTQQIPPAYK
	550	560	570	580	590
mouse	DLAEFWIQVF	GMELVGCLFS	RNNVREMAI	RRLSHDVSGA	LLLANGESTG
human	DLAEFWIQVF	GMELVGCLFS	RNNVREMAI	RRLSHDVSGA	LLLANGESTG
	600	610	620	630	640
mouse	NSGGGSGGSL	SAGAASGSSQ	PSISGDVVEA	CCSVLSIVCA	DPVKVYVAA
human	NSGGGSGGSL	SAGAASGSSQ	PSISGDVVEA	CCSVLSIVCA	DPVKVYVAA
	650	660	670	680	690
mouse	LKTLRAMLVY	TPCHSLAERI	KLQRLRPVW	DTILVKCADA	NSRTSQLSIS
human	LKTLRAMLVY	TPCHSLAERI	KLQRLRPVW	DTILVKCADA	NSRTSQLSIS
	700	710	720	730	740
mouse	TVLELCKGQA	GELAVGREIL	KAGSIGVGGV	DYVLSCILGN	QAESNNWQEL
human	TVLELCKGQA	GELAVGREIL	KAGSIGVGGV	DYVLSCILGN	QAESNNWQEL
	750	760	770	780	790
mouse	LGRICLIDRL	LLEFPAEFYP	HIVSTDVSQA	EPVEIRYKKL	LSLLTFALQS
human	LGRICLIDRL	LLEFPAEFYP	HIVSTDVSQA	EPVEIRYKKL	LSLLTFALQS
	800	810	820	830	840
mouse	IDNSHSMVGK	LSRRIYLSSA	RMVTAVPAVF	SKLVIMLNAS	GSIHFTRMRR
human	IDNSHSMVGK	LSRRIYLSSA	RMVTAVPAVF	SKLVIMLNAS	GSIHFTRMRR
	850	860	870	880	890
mouse	RLMAIADEVE	IAEVIQLGVE	DTVDGHQDSL	QAVAPTSCLE	NSSLEHTVHR
human	RLMAIADEVE	IAEVIQLGVE	DTVDGHQDSL	QALAPASCLE	NSSLEHTVHR

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FIGURE 3B

	900	910	920	930	940
mouse	EKTGKGLSAT	RLSASSEDIS	DRLAGVSVGL	PSSTITTEQPK	PAVQTKGRPH
human	EKTGKGLSAT	RLSASSEDIS	DRLAGVSVGL	PSSTITTEQPK	PAVQTKGRPH
	950	960	970	980	990
mouse	SQCLNSSPLS	HAQLMFPPAPS	APCSSAPSVP	DISKHRPQAF	VPCKIPSPASP
human	SQCLNSSPLS	HAQLMFPPAPS	APCSSAPSVP	DISKHRPQAF	VPCKIPSPASP
	1000	1010	1020	1030	1040
mouse	QTQRKFSLOF	QRNCSEHRDS	DQLSPVFTQS	RPPPSNNIHR	PKPSRPVFGS
human	QTQRKFSLOF	QRNCSEHRDS	DQLSPVFTQS	RPPPSNNIHR	PKPSRPVFGS
	1050	1060	1070	1080	1090
mouse	TSKLGDAIKS	SMTLDLGSAS	RCDDSFSGGGG	NSGNAVIPSD	ETVFTFVEDK
human	TSKLGDAIKS	SMTLDLGSAS	RCDDSFSGGGG	NSGNAVIPSD	ETVFTFVEDK
	1100	1110	1120	1130	1140
mouse	CRLDVNTELN	SSIEDLLEAS	MPSSDITVIF	KSEVAVLSPE	KAENDDTYKD
human	CRLDVNTELN	SSIEDLLEAS	MPSSDITVIF	KSEVAVLSPE	KAENDDTYKD
	1150	1160	1170	1180	1190
mouse	DVNHNQKCKE	KMEAEEEEFAL	AIAMAMSASQ	DALPIVPQLQ	VENGEDIIII
human	DVNHNQKCKE	KMEAEEEEFAL	AIAMAMSASQ	DALPIVPQLQ	VENGEDIIII
	1200	1210	1220	1230	1240
mouse	QQDTPETLPG	HTKAKQPYRE	DAEWLKGQOI	GLGAFSSCYQ	AQDVGIGTLM
human	QQDTPETLPG	HTKAKQPYRE	DAEWLKGQOI	GLGAFSSCYQ	AQDVGIGTLM
	1250	1260	1270	1280	1290
mouse	AVKQVTYVRN	TSSEQEEVVE	ALREEIRMMG	HLNHPNIIRM	LGATCEKSNY
human	AVKQVTYVRN	TSSEQEEVVE	ALREEIRMMG	HLNHPNIIRM	LGATCEKSNY
	1300	1310	1320	1330	1340
mouse	NLFIEWMAGG	SVAHLLSKYG	AFKESVVINY	TEQLLRGLSY	LHENQIIHRD
human	NLFIEWMAGG	SVAHLLSKYG	AFKESVVINY	TEQLLRGLSY	LHENQIIHRD

FIGURE 3C



### hMEKK1/mMEKK1 Protein Alignment

	1350	1360	1370	1380	1390
mouse	VKGANLLIDS	TGQRLRIADF	GAAARLASKG	TGAGEFQQQL	LGTTAFMAPE
human	VKGANLLIDS	TGQRLRIADF	GAAARLASKG	TGAGEFQQQL	LGTTAFMAPE
	1400	1410	1420	1430	1440
mouse	VLRGQQYGRS	CDVWSVGCAI	IEMACAKPPW	NAEKHSNHLA	LIFKIASATT
human	VLRGQQYGRS	CDVWSVGCAI	IEMACAKPPW	NAEKHSNHLA	LIFKIASATT
	1450	1460	1470	1480	1490
mouse	APSIPSHLSP	GLRDVAVRCL	ELQPQDRPPS	RELLKHPVFR	TTW*
human	APSIPSHLSP	GLRDVALRCL	ELQPQDRPPS	RELLKHPVFR	TTW*

FIGURE 3D

$\alpha$	$\beta$	$\gamma$	$\delta$	$\epsilon$	$\zeta$	$\eta$	$\theta$	$\iota$	$\kappa$	$\lambda$	$\mu$	$\nu$	$\xi$	$\omicron$	$\pi$	$\rho$	$\sigma$	$\tau$	$\upsilon$	$\phi$	$\chi$	$\psi$	$\omega$	
0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5

FIG.4

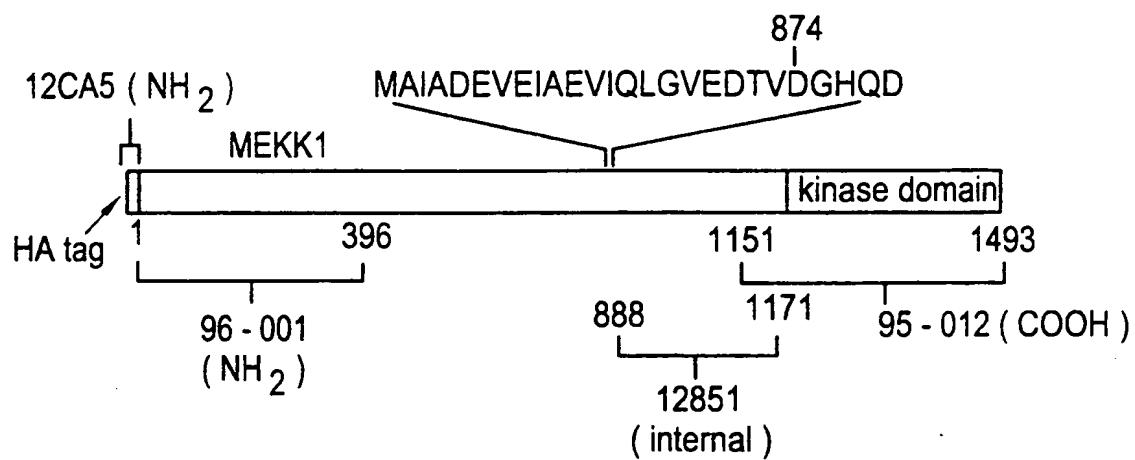
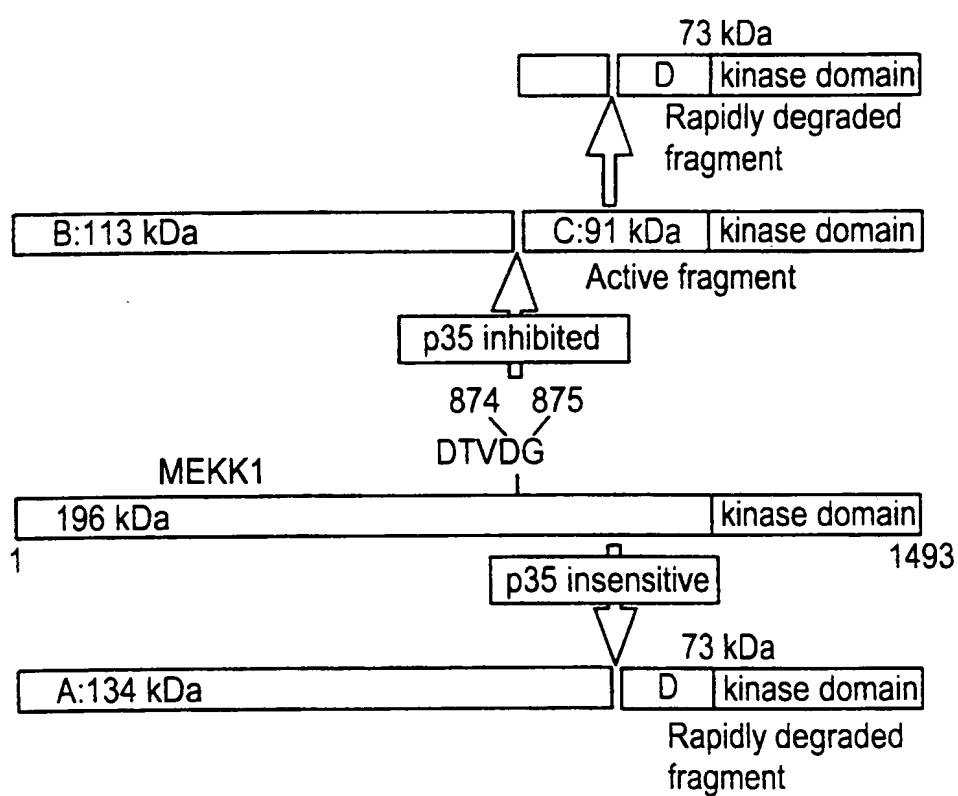
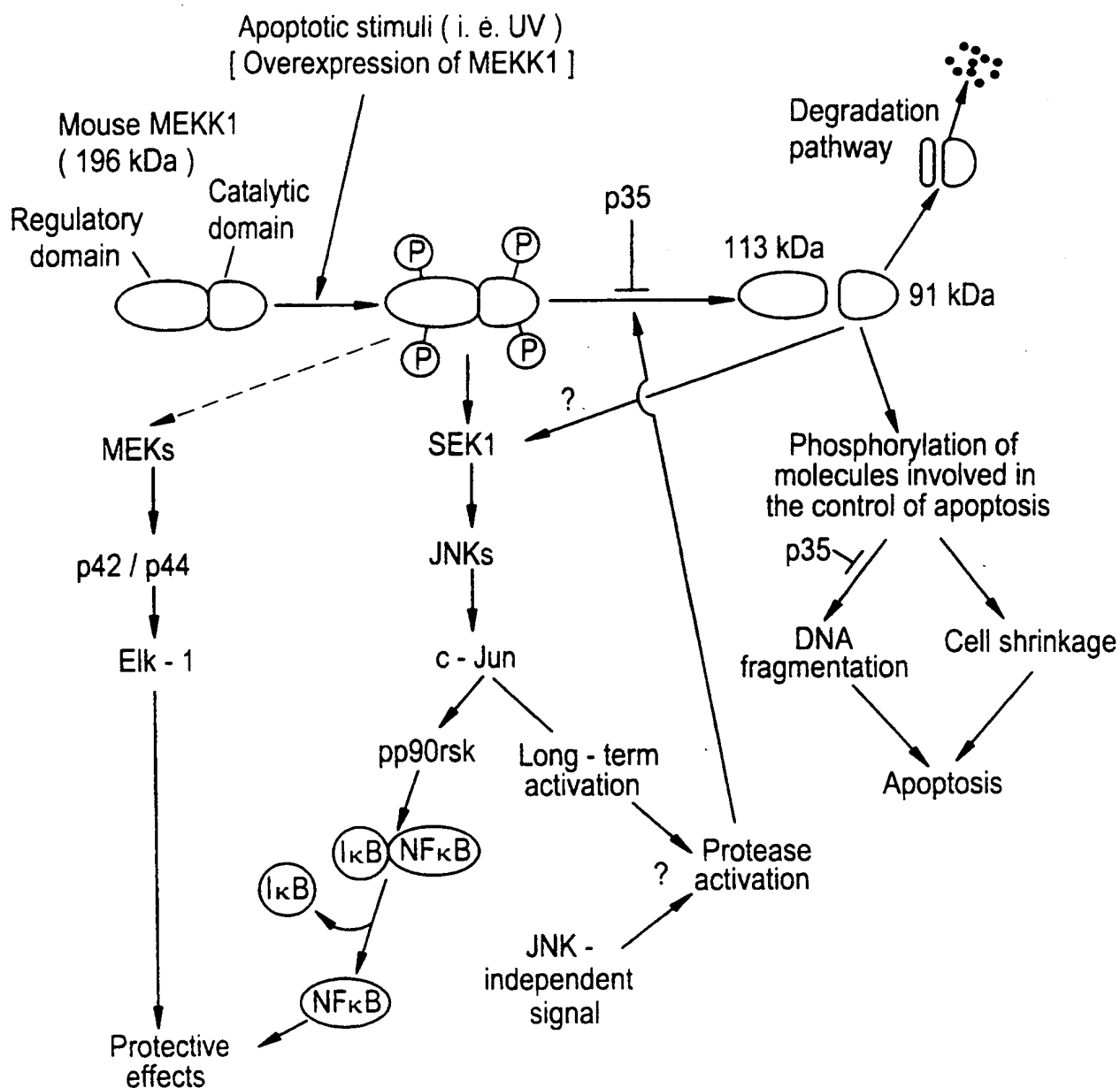


FIG.5



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FIG.6



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## Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

	Similarity Index	Gap Number	Gap Length	Consensus Length
(1>1493)	94.1	4	10	1498
(1>1493)				
NSGGGSGGSL SAGAASGSSQPSISGDVVEACCSVLSIVCADPVYKVYVAALKTLRAMLVY				
TSGGGSGGSL SAGAASGSSQPSISGDVVEAFCSVLSIVCADPVYKVYVAALKTLRAMLVY				
TPCHSLAERIKLQRLRPVVDITLVKCADANSRTSQLSISTVLELCKGOAGELAVGREIL				
TPCHSLAERIKLQRLRPVVDITLVKCADANSRTSQLSISTLLELCKGOAGELAVGREIL				
KAGSIGVGGVDYVLSCLGNQAESNNWQELLGRCLIDRLLLEFPAEFYPHIVSTOVSQA				
KAGSIGVGGVDYVLSCLGNQAESNNWQELLGRCLIDRLLLEISAEFYPHIVSTOVSQA				
EPVEIRYKKLLSLLTFALOSIDNSHSMVGKLSRRILYSSARMVTAVPAVFSKLVTLNLS				
EPVEIRYKKLLSLLAFALOSIDNSHSMVGKLSRRILYSSARMVTTVPPLFSKLVTLNLS				
GSTHFTMRMRRLMAIADEVEIAEVIQLGVEDTVDGHQDSLOAVAPTSCLENSLEHTVHR				
GSSHFAARMRRRLMAIADEVEIAEVIQLGSEDTLDGQDSSQALAPPRYPRESSLEHTAHV				
EKTGKGLSATRLSASSEDISDRLAGYSVGLPSSSTTTEQPKPAVQTKGRPHSQCLNSSLPS				
EKTGKGLKATRLSASSEDISDRLAGYSVGLPSSATTEQPKPTVQTKGRPHSQCLNSSLPS				
HAQLMFAPAPSAPCSSAPSVP-----DISKHRPQAFVPCKIPSASPQTQRKFSLOFQRNCS				
PPQLMFPAISAPCSSAPSVPAGSVTDASKHRPRAFPVCKIPSASPQTQRKFSLOFQRTCS				
EHRDSQQLSPVFTQSRPPSSNIHRPKPSRPVPGSTSKLGDATKSSMTLDLGSASRCDDS				
ENRDSEKLSPVFTQSRPPSSNIHRKASRPVPGSTSKLGDASKNSMTLDLNSASQCDDS				
FGGGGNSGNAVIPSDETFTVPTVEDKCRLOVNTLNSSIEDLLEASMPSSDTTTFKSEVA				
FGSGSNSGSAVIPSEETAFTPAEDKCRLOVNPENLNSSIEDLLEASMPSSDTTTFKSEVA				
VLSPEKAENDDTYKDDVNHNOCKEKEAEEEEALAIAMAMSASQDALPIVPOLQVENGE				
VLSPEKAESDDTYKDDVNHNOCKEKEAEEEEALAIAMAMSASQDALPIVPOLQVENGE				

FIGURE 7A

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## Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

	Similarity Index	Gap Number	Gap Length	Consensus Length
(1>1493)	(1>1493)	94.1	4	10
MAAAAGDRASSSGFPGAAAAASPEAGGGGGGGGALOGSGAPAAGAAGLLREPGSAGRERAD				1498
MAAAAGDRASSSGFPGAAAAASPEA---GGGGGALOGSGAPAAGA-GLLRETGSAGRERAD				
WRRQRLRKVRSVELDQLPEQPLFLAAASPPCPSTSPSPPEPADAAGASRFQPAAGPPPPG				
WRRQRLRKVRSVELDQLPEQPLFLTA-SPPCPSTSPSPPEPADAAGASGFQPAAGPPPPG				
AASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMENKETLKGLHKMEDRPEERMI				
AASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMENKETLKGLHKMDDRPEERMI				
REKLKATCMPAWKHEWLERRNRRGPVVVKPIPIKGDGSEVNNLAAEPOGEGQAGSAAPAP				
REKLKATCMPAWKHEWLERRNRRGPVVVKPIPIKGDGSEMSNLAELQEGQAGSAAPAP				
KGRRSPSPGSSPSGRSVKPESPGYRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETS				
KGRRSPSPGSSPSGRSGKPESPGYRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETS				
RRVNVKMRARLYLLQOIGPNSFLIGGDSPODKYRVFIGPONCSCGRGAFCHLLFVMLRV				
RRVNVKMRARLYLLQOIGPNSFLIGGDSPODKYRVFIGPONCSCGRGTFCIHLFVMLRV				
FQLEPSDPMLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIOKFVSRMSNSHTLSSSS				
FQLEPSDPMLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIOKFVSRMSNCHTLSSSS				
TSTSSSENSIKDEEEOMCPICLLGMLDEESLTVCEGDCRNKLHHHCMSIWAECCRNRREP				
TSTSSSENSIKDEEEOMCPICLLGMLDEESLTVCEGDCRNKLHHHCMSIWAECCRNRREP				
LICPLCRSKWRSHDFYSHELSSPVESPAASLRAVQOPSSPQOPVAGSQRNRNOESSFNLTHTF				
LICPLCRSKWRSHDFYSHELSSPVDSPSLRGVQOPSSPQOPVAGSQRNRNOESNLTHTY				
GTQOIPSAKYDLAEPWIOVFGMELVGCLFSRNWNVREMARRLSHOVSGALLANGESTG				
GTQOIPPAYKDLAEPWIOAFGMELVGCLFSRNWNVREMARRLSHOVSGALLANGESTG				

FIGURE 7B

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f

## Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

		Similarity Index	Gap Number	Gap Length	Consensus Length
(1>1493)	(1>1493)	94.1	4	10	1498
↖1200	↖1210	↖1220	↖1230	↖1240	↖1250
DI III I OODTPETLPGHTKAKOPYREDAEWLKGQO IGLGAFSSCYQAQDVGTGTLMAVKOV					
DI III I OODTPETLPGHTKANEPYREDTEWLKGQO IGLGAFSSCYQAQDVGTGTLMAVKOV					
↖1200	↖1210	↖1220	↖1230	↖1240	↖1250
↖1260	↖1270	↖1280	↖1290	↖1300	↖1310
TYVRNTSSEQEEVVEALREE I RMMGHLNHPNI I RMLGATCEKSNYNLF I EWMAGGSVAHL					
TYVRNTSSEQEEVVEALREE I RMMSHLNHPNI I RMLGATCEKSNYNLF I EWMAGASVAHL					
↖1260	↖1270	↖1280	↖1290	↖1300	↖1310
↖1320	↖1330	↖1340	↖1350	↖1360	↖1370
LSKYGAFKESVVINYTEQLLRGLSYLHENQ I IHRDVKGANLL I DSTGQRLRIADFGAAAR					
LSKYGAFKESVVINYTEQLLRGLSYLHENQ I IHRDVKGANLL I DSTGQRLRIADFGAAAR					
↖1320	↖1330	↖1340	↖1350	↖1360	↖1370
↖1380	↖1390	↖1400	↖1410	↖1420	↖1430
LASKGTGAGEFQGOLLGT I AFMAPEVLRGQOYGRSCDVWSVGCAI I EMACAKPPWNAEKH					
LASKGTGAGEFQGOLLGT I AFMAPEVLRGQOYGRSCDVWSVGCAI I EMACAKPPWNAEKH					
↖1380	↖1390	↖1400	↖1410	↖1420	↖1430
↖1440	↖1450	↖1460	↖1470	↖1480	↖1490
SNHLALIFKIASATTAPSI PSHLSPGLRDVAVRCLELQPD RPPSRELLKHPVFR TTW					
SNHLALIFKIASATTAPSI PSHLSPGLRDVALRCLELQPD RPPSRELLKHPVFR TTW					
↖1440	↖1450	↖1460	↖1470	↖1480	↖1490

FIGURE 7C

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## MEKK 1

rat	MAAAAGDRASSSGFPGAAAASPEA---GGGGGALQGSQAPAAG-AGLLRETGSAGRE
mouse	MAAAAGDRASSSGFPGAAAASPEAGGGGGGGGALQGSQAPAAGAAGLLREPGSAGRE
rat	RADWRRQQLRKVRSVELDQLPEQPLFL-TASPPCPSTSPSPPEPADAAGASGFQPA
mouse	RADWRRQQLRKVRSVELDQLPEQPLFLAAASPPCPSTSPSPBPADAAGASRFQPA
rat	GPPPPGAASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMEKTKGLHKM
mouse	GPPPPGAASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMEKTKGLHKM
rat	DDRPEERMIREKLKATCMPAWKHEWLERRNRRGFVVVKPIPIKGDGSEMSNLAAELQ
mouse	EDRPEERMIREKLKATCMPAWKHEWLERRNRRGFVVVKPIPIKGDGSEVNNLAAEPQ
rat	GEGQAGSAAPAPKGRRSPSPGSSPSGRSGKPESPGVRRKRVSFVFFQSGRITPPRRA
mouse	GEGQAGSAAPAPKGRRSPSPGSSPSGRSVKPESPGVRRKRVSFVFFQSGRITPPRRA
rat	PSPDGFSPYSPEETSRRVNKVMRRLYLLOQIGPNSFLIGGDSFDNKYRVFIGPQNC
mouse	PSPDGFSPYSPEETSRRVNKVMRRLYLLOQIGPNSFLIGGDSFDNKYRVFIGPQNC
rat	SCGRGTFCIHLFVMLRVFQLEPSDFMLWRKTLKNFEVESLFQKYHSRRSSRIKAPS
mouse	SCGRGAFCIHLFVMLRVFQLEPSDFMLWRKTLKNFEVESLFQKYHSRRSSRIKAPS
rat	RNTIQKFVSRMSNCHTLSSSSTSTSSSENSIKDEEEQMCPICLLGMLEESLTVCE
mouse	RNTIQKFVSRMSNCHTLSSSSTSTSSSENSIKDEEEQMCPICLLGMLEESLTVCE
rat	GCRNKLHHHCMSIWAEECRNRNREPLICPLCRSKWRSHDFYSHELSSPVDSPSTSLRGV
mouse	GCRNKLHHHCMSIWAEECRNRNREPLICPLCRSKWRSHDFYSHELSSPVESPASLRAV
human	NKLHHHCMSIWAEECRNRN PLICPLCRS WRSHDFYSHELSSPVDSPSSL
rat	QQPSSPOQPVAGSQRRNQESFNLTHTYGTQQIPFAYKDLAEPWQVFGMELVGCCLFS
mouse	QQPSSPOQPVAGSQRRNQESSFNLTHTYGTQQIPFAYKDLAEPWQVFGMELVGCCLFS
human	Q V HPLAGS RRNQESFNLTHTYGTQQIPFAYKDLAEPWQVFGMELVGCCLFS
rat	RNWNVREMA LRRLSHDVSGALLANGESTGTSGGGSGGSLSAGAASGSSQPSISGDV
mouse	RNWNVREMA LRRLSHDVSGALLANGESTGNSGGSGGSLSAGAASGSSQPSISGDV
human	RNWNVREMA LRRLSHDVSGALLANGESTGNSGGSGGSSPSGGATSG SQTS SGD
rat	VEAFCSVLSIVCADPVYKVYVAALKTLRAMLVYTPCHSLAERIKLQRLLRPVVDLIL
mouse	VEACCSVLSIVCADPVYKVYVAALKTLRAMLVYTPCHSLAERIKLQRLLRPVVDLIL
human	VEACC
rat	VKCADANSRTSQLSISTVLELCKGQAGELAVGREILKAGSIGVGGVDYVLSLILGNQ
mouse	VKCADANSRTSQLSISTVLELCKGQAGELAVGREILKAGSIGVGGVDYVLSLILGNQ
human	
rat	AESNNWQELLGRCLIDRLLEISAEFYPHIVSTDVSQAEFVEIRYKLLSLLAFAL
mouse	AESNNWQELLGRCLIDRLLEFPAEFYPHIVSTDVSQAEFVEIRYKLLSLLTFAL
human	PAEFYPHIVSTDVSQAEFVEIRYKLLSLL FA
rat	QSIDNSHSMVGKLSRRIYLSSARMVTVPPPIFSKLVTMLNAGSSHFARMRRRLMAI
mouse	QSIDNSHSMVGKLSRRIYLSSARMVTA VPAVFSKLVTMLNAGSTHFTMRRLMAI
human	K ID SHSMVG SR DISLCYDDGRSAVCPPSW PCLMLLGSTHFTMRRLMAI

FIGURE 8A

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rat	ADEVEIAEVIQLGSEDTLDGQQDSSQALAPPRYPSSSLEHTAHVEKTGKGLKATRL
mouse	ADEVEIAEVIQLGVEDTVDGHQDSLQAVAPTSCLENSLEHTVHREKTGKGLSATRL
human	ADEVIAEVIQLGEVDTVDGHQDSLRLALAPASCRENSLEHTVHREKTGKGLSATRL
rat	SASSEDISDRLAGVSVGLPSSATTEQPKPTVQTKGRPHSQCLNSSPLSPPQLMFPAT
mouse	SASSEDISDRLAGVSVGLPSSSTTTEQPKPAVQTKGRPHSQCLNSSPLSHAQLMFPAP
human	STSSEEISDRLAGVSVGFPSSTTTEQPKPAVQTKGRPHSQCLNSSPLSHAQLMFPAP
rat	SAPCSSAPSVPAAGSVTDASKHRPRAFPVCKIPASAPQTKRKFSLQFQRTCSNRDSE
mouse	SAPCSSAPSVP-----DISKHPQAFVPCIPASAPQTKRKFSLQFQRNCSEHRDSD
human	SAPCSSAP VP DISKHPQAFVPCILPHLPQTKRKFSLQFQRN EHRDQT
rat	KLSPVFTQSRPPSSNIHRAKASRPVPGSTSKLGDASKNSMTLDLNSASQCDDSFSGS
mouse	QLSPVFTQSRPPSSNIHRPKSRPVPGSTSKLGDATKSSMTLDLGSASRCDDSFQGG
human	QLSPVFTQSQDPTSSNIHRPKDRPAPGSTSKLGDATKSSMTLDLGCRCDDSFQGG
rat	GSNSGSAVIPSEETAFTPAEDKCRLDVNPENSSIEDLLEASMPSSDTTVTFKSEVA
mouse	GGNSGSAVIPSDETVFTPVEDKCRLDVNTENSSIEDLLEASMPSSDTTVTFKSEVA
human	GGNSGSAVIPSDETVFTPVEDKCRLDVNTENSSIEDLLEASMPSSDTTVTFKSEVA
rat	VLSPEKAESDDTYKDDVNHNNQCKEKEAEAEAEALAMAMSASQDALPIVPQLQVE
mouse	VLSPEKAENDDTYKDDVNHNNQCKEKEAEAEAEALAMAMSASQDALPIVPQLQVE
human	VLSPEKAENDDTYK VY
rat	NGEDIIIIQQDTPETLPGHTKANEPYREDTEWLKGOQIGLGFSSCYQAQDVGTGTL
mouse	NGEDIIIIQQDTPETLPGHTKAKQPYREDAEWLKGQOIGLGFSSCYQAQDVGTGTL
human	VIQQDTPETLPGHTKAKQPYREDAEWL G QIGLGHF
rat	MAVKQVTYVRNTSSEQEEVVEALREEIRMMSHLNHPNIIIRMLGATCEKSNYNLFIEW
mouse	MAVKQVTYVRNTSSEQEEVVEALREEIRMMGHLNHPNIIIRMLGATCEKSNYNLFIEW
human	EEIR MSHLNHP IIRMLG TGKKNY LFIEW
rat	MAGASVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQ
mouse	MAGGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQ
human	MAGGSVAHLLSKYGAF ESIVI YTEQ LRGLSYLHENQIIH DVKGANLLID TG
rat	RLRIADFGAAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQOYGRSCDVWSVGCAI
mouse	RLRIADFGAAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQOYGRSCDVWSVGCAI
human	RLRIADFGAAA LASKG GAGEFQGL GTIAFMAPEV RG QYGRSCDVWSVGCAI
rat	IEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPLGRDVALRCLELQPQDR
mouse	IEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPLGRDVAVRCLLELQPQDR
human	IEMACAKPPWNAEKHSNHLALIKKIASATTAPSIPSHLSPLGRNVALRCLELQPQDR
rat	PPSRELLKHPVFRTTW
mouse	PPSRELLKHPVFRTTW
human	PPSRELLKHPVFRTT

FIGURE 8B

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